

#3

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/903,063

DATE: 10/30/2001

TIME: 11:59:43

Input Set : A:\Rih32d31.app

Output Set: N:\CRF3\10302001\I903063.raw

3 <110> APPLICANT: Wands, Jack R.
4 de la Monte, Suzanne M.
5 Ince, Nedim
6 Carlson, Rolf I.
8 <120> TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF MALIGNANT NEOPLASMS
10 <130> FILE REFERENCE: 21486-032 DIV3
12 <140> CURRENT APPLICATION NUMBER: 09/903,063
C--> 13 <141> CURRENT FILING DATE: 2001-10-11 *ok*
15 <150> PRIOR APPLICATION NUMBER: 09/436,184
16 <151> PRIOR FILING DATE: 1999-11-08
18 <160> NUMBER OF SEQ ID NOS: 9
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 36
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus
29 EGF-like domain
31 <220> FEATURE:
32 <221> NAME/KEY: VARIANT
33 <222> LOCATION: (2)..(8)
34 <223> OTHER INFORMATION: Wherein Xaa is any amino acid ✓
36 <220> FEATURE:
37 <221> NAME/KEY: VARIANT
38 <222> LOCATION: (10)..(13)
39 <223> OTHER INFORMATION: Wherein Xaa is any amino acid. ✓
41 <220> FEATURE:
42 <221> NAME/KEY: VARIANT
43 <222> LOCATION: (15)..(24)
44 <223> OTHER INFORMATION: Wherein Xaa is any amino acid. ✓
46 <220> FEATURE:
47 <221> NAME/KEY: VARIANT
48 <222> LOCATION: (26)
49 <223> OTHER INFORMATION: Wherein Xaa is any amino acid. ✓
51 <220> FEATURE:
52 <221> NAME/KEY: VARIANT
53 <222> LOCATION: (28)..(35)
54 <223> OTHER INFORMATION: Wherein Xaa is any amino acid. ✓
56 <400> SEQUENCE: 1
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58 1 5 10 15
W--> 60 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa
61 20 25 30
W--> 63 Xaa Xaa Xaa Cys
64 35
67 <210> SEQ ID NO: 2

ENTERED

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68 <211> LENGTH: 758
69 <212> TYPE: PRT
70 <213> ORGANISM: Homo sapiens
72 <400> SEQUENCE: 2
73 Met Ala Gln Arg Lys Asn Ala Lys Ser Ser Gly Asn Ser Ser Ser Ser
74   1           5           10           15
76 Gly Ser Gly Ser Gly Ser Thr Ser Ala Gly Ser Ser Ser Pro Gly Ala
77           20           25           30
79 Arg Arg Glu Thr Lys His Gly Gly His Lys Asn Gly Arg Lys Gly Gly
80           35           40           45
82 Leu Ser Gly Thr Ser Phe Phe Thr Trp Phe Met Val Ile Ala Leu Leu
83           50           55           60
85 Gly Val Trp Thr Ser Val Ala Val Val Trp Phe Asp Leu Val Asp Tyr
86   65           70           75           80
88 Glu Glu Val Leu Gly Lys Leu Gly Ile Tyr Asp Ala Asp Gly Asp Gly
89           85           90           95
91 Asp Phe Asp Val Asp Asp Ala Lys Val Leu Leu Gly Leu Lys Glu Arg
92           100          105          110
94 Ser Thr Ser Glu Pro Ala Val Pro Pro Glu Glu Ala Glu Pro His Thr
95           115          120          125
97 Glu Pro Glu Glu Gln Val Pro Val Glu Ala Glu Pro Gln Asn Ile Glu
98           130          135          140
100 Asp Glu Ala Lys Glu Gln Ile Gln Ser Leu Leu His Glu Met Val His
101 145           150           155           160
103 Ala Glu His Val Glu Gly Glu Asp Leu Gln Gln Glu Asp Gly Pro Thr
104           165           170           175
106 Gly Glu Pro Gln Gln Glu Asp Asp Glu Phe Leu Met Ala Thr Asp Val
107           180           185           190
109 Asp Asp Arg Phe Glu Thr Leu Glu Pro Glu Val Ser His Glu Glu Thr
110           195           200           205
112 Glu His Ser Tyr His Val Glu Glu Thr Val Ser Gln Asp Cys Asn Gln
113           210           215           220
115 Asp Met Glu Glu Met Met Ser Glu Gln Glu Asn Pro Asp Ser Ser Glu
116 225           230           235           240
118 Pro Val Val Glu Asp Glu Arg Leu His His Asp Thr Asp Asp Val Thr
119           245           250           255
121 Tyr Gln Val Tyr Glu Glu Gln Ala Val Tyr Glu Pro Leu Glu Asn Glu
122           260           265           270
124 Gly Ile Glu Ile Thr Glu Val Thr Ala Pro Pro Glu Asp Asn Pro Val
125           275           280           285
127 Glu Asp Ser Gln Val Ile Val Glu Glu Val Ser Ile Phe Pro Val Glu
128           290           295           300
130 Glu Gln Gln Glu Val Pro Pro Glu Thr Asn Arg Lys Thr Asp Asp Pro
131 305           310           315           320
133 Glu Gln Lys Ala Lys Val Lys Lys Lys Lys Pro Lys Leu Leu Asn Lys
134           325           330           335
136 Phe Asp Lys Thr Ile Lys Ala Glu Leu Asp Ala Ala Glu Lys Leu Arg
137           340           345           350
139 Lys Arg Gly Lys Ile Glu Glu Ala Val Asn Ala Phe Lys Glu Leu Val

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140	355	360	365
142 Arg Lys Tyr Pro Gln Ser	Pro Arg Ala Arg Tyr Gly Lys Ala Gln Cys		
143 370	375	380	
145 Glu Asp Asp Leu Ala Glu Lys Arg Arg Ser Asn Glu Val Leu Arg Gly			
146 385	390	395	400
148 Ala Ile Glu Thr Tyr Gln Glu Val Ala Ser Leu Pro Asp Val Pro Ala			
149 405	410	415	
151 Asp Leu Leu Lys Leu Ser Leu Lys Arg Arg Ser Asp Arg Gln Gln Phe			
152 420	425	430	
154 Leu Gly His Met Arg Gly Ser Leu Leu Thr Leu Gln Arg Leu Val Gln			
155 435	440	445	
157 Leu Phe Pro Asn Asp Thr Ser Leu Lys Asn Asp Leu Gly Val Gly Tyr			
158 450	455	460	
160 Leu Leu Ile Gly Asp Asn Asp Asn Ala Lys Lys Val Tyr Glu Glu Val			
161 465	470	475	480
163 Leu Ser Val Thr Pro Asn Asp Gly Phe Ala Lys Val His Tyr Gly Phe			
164 485	490	495	
166 Ile Leu Lys Ala Gln Asn Lys Ile Ala Glu Ser Ile Pro Tyr Leu Lys			
167 500	505	510	
169 Glu Gly Ile Glu Ser Gly Asp Pro Gly Thr Asp Asp Gly Arg Phe Tyr			
170 515	520	525	
172 Phe His Leu Gly Asp Ala Met Gln Arg Val Gly Asn Lys Glu Ala Tyr			
173 530	535	540	
175 Lys Trp Tyr Glu Leu Gly His Lys Arg Gly His Phe Ala Ser Val Trp			
176 545	550	555	560
178 Gln Arg Ser Leu Tyr Asn Val Asn Gly Leu Lys Ala Gln Pro Trp Trp			
179 565	570	575	
181 Thr Pro Lys Glu Thr Gly Tyr Thr Glu Leu Val Lys Ser Leu Glu Arg			
182 580	585	590	
184 Asn Trp Lys Leu Ile Arg Asp Glu Gly Leu Ala Val Met Asp Lys Ala			
185 595	600	605	
187 Lys Gly Leu Phe Leu Pro Glu Asp Glu Asn Leu Arg Glu Lys Gly Asp			
188 610	615	620	
190 Trp Ser Gln Phe Thr Leu Trp Gln Gln Gly Arg Arg Asn Glu Asn Ala			
191 625	630	635	640
193 Cys Lys Gly Ala Pro Lys Thr Cys Thr Leu Leu Glu Lys Phe Pro Glu			
194 645	650	655	
196 Thr Thr Gly Cys Arg Arg Gly Gln Ile Lys Tyr Ser Ile Met His Pro			
197 660	665	670	
199 Gly Thr His Val Trp Pro His Thr Gly Pro Thr Asn Cys Arg Leu Arg			
200 675	680	685	
202 Met His Leu Gly Leu Val Ile Pro Lys Glu Gly Cys Lys Ile Arg Cys			
203 690	695	700	
205 Ala Asn Glu Thr Arg Thr Trp Glu Glu Gly Lys Val Leu Ile Phe Asp			
206 705	710	715	720
208 Asp Ser Phe Glu His Glu Val Trp Gln Asp Ala Ser Ser Phe Arg Leu			
209 725	730	735	
211 Ile Phe Ile Val Asp Val Trp His Pro Glu Leu Thr Pro Gln Gln Arg			
212 740	745	750	

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214 Arg Ser Leu Pro Ala Ile

215 755

218 <210> SEQ ID NO: 3

219 <211> LENGTH: 2324

220 <212> TYPE: DNA

221 <213> ORGANISM: Homo sapiens

223 <400> SEQUENCE: 3

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224 cggaccgtgc aatggcccag cgtaagaatg ccaagagcag cggcaacagc agcagcagcg 60
225 gctccggcag cggtagcacg agtgcggggc gcagcagccc cggggcccgg agagagacaa 120
226 agcatggagg acacaagaat gggaggaaa ggcgactctc ggaacttca ttcttcacgt 180
227 ggtttatggg gattgcattg ctgggcgtct ggacatctgt agctgtcgtt tggtttgatc 240
228 ttgttgacta tgaggaaagt ctaggaaaac taggaatcta tgatgctgat ggtgatggag 300
229 attttgatgt ggatgatgcc aaagttttat taggaactaa agagagatct acttcagagc 360
230 cagcagtccc gccagaagag gctgagccac aactgagcc cgaggagcag gttcctgtgg 420
231 aggcagaacc ccagaatatc gaagatgaag caaaaagaaca aattcagtcc cttctccatg 480
232 aaatggtaca cgcagaacat gttgagggag aagacttgca acaagaagat ggaccacag 540
233 gagaaccaca acaagaggat gatgagtttc ttatggcgac tgatgtagat gatagatttg 600
234 agaccctgga acctgaagta tctcatgaag aaaccgagca tagttaccac gtggaagaga 660
235 cagtttcaca agactgtaat caggatatgg aagagatgat gtctgagcag gaaaatccag 720
236 attccagtga accagtagta gaagatgaaa gattgcacca tgatacagat gatgtaacat 780
237 accaagtcta tgaggaacaa gcagtatatg aacctctaga aaatgaaggg atagaaatca 840
238 cagaagtaac tgctccccct gaggataatc ctgtagaaga ttcacaggta attgtagaag 900
239 aagtaagcat ttttcctgtg gaagaacagc aggaagtacc accagaaaca aatagaaaaa 960
240 cagatgatcc agaacaaaaa gcaaaaagta agaaaaagaa gcctaaactt ttaaataaat 1020
241 ttgataagac tattaagct gaacttgatg ctgcagaaaa actccgtaa aggggaaaaa 1080
242 ttgaggaagc agtgaatgca tttaaagaac tagtacgcaa ataccctcag agtccacgag 1140
243 caagatatgg gaaggcgag tgtgaggatg atttggtga gaagaggaga agtaatgagg 1200
244 tgctacgtgg agccatcgag acctaccaag aggtggccag cctacctgat gtccctgcag 1260
245 acctgctgaa gctgagtttg aagcgctcgt cagacaggca acaatttcta ggtcatatga 1320
246 gaggtttcct gcttaccctg cagagattag ttcaactatt tcccaatgat acttccttaa 1380
247 aaaatgacct tggcggtggg tacctcttga taggagataa tgacaatgca aagaaagttt 1440
248 atgaagaggt gctgagtgtg acacctaatg atggctttgc taaagtccat tatggcttca 1500
249 tcctgaaggc acagaacaaa attgctgaga gcatcccata tttaaaggaa ggaatagaat 1560
250 ccggagatcc tggcactgat gatgggagat tttatttcca cctgggggat gccatgcaga 1620
251 gggttgggaa caaagaggca tataagtgg atgagcttgg gcacaagaga ggacactttg 1680
252 catctgtctg gcaacgctca ctctacaatg tgaatggact gaaagcacag ccttgggtgga 1740
253 cccaaaaga aacgggctac acagagttag taaagtcttt agaaagaaac tggaggttaa 1800
254 tccgagatga aggccttgca gtgatggata aagccaaagg tctcttcctg cctgaggatg 1860
255 aaaacctgag ggaaaaaggg gactggagcc agttcacgct gtggcagcaa ggaagaagaa 1920
256 atgaaaatgc ctgcaaagga gctcctaaaa cctgtacctt actagaaaag ttccccgaga 1980
257 caacaggatg cagaagagga cagatcaaat attccatcat gcaccccggg actcacgtgt 2040
258 ggccgcacac agggcccaca aactgcaggc tccgaatgca cctgggcttg gtgattccca 2100
259 aggaaggctg caagattcga tgtgccaacg agaccaggac ctgggaggaa ggcaagggtg 2160
260 tcacttttga tgactccttt gagcacgagg tatggcagga tgccatctt ttccggctga 2220
261 tattcatcgt ggatgtgtgg catccggaac tgacaccaca gcagagacgc agccttccag 2280
262 caatttagca tgaattcatg caagcttggg aaactctgga gaga 2324

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265 <210> SEQ ID NO: 4

266 <211> LENGTH: 31

267 <212> TYPE: PRT

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Input Set : A:\Rih32d31.app

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268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: Description of Artificial Sequence: EGF-like
272     cysteine-rich repeat
274 <220> FEATURE:
275 <221> NAME/KEY: VARIANT
276 <222> LOCATION: (3)..(5)
277 <223> OTHER INFORMATION: Wherein any Xaa may be any amino acid ✓
279 <220> FEATURE:
280 <221> NAME/KEY: VARIANT
281 <222> LOCATION: (6)..(7)
282 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
284 <220> FEATURE: ✓
285 <221> NAME/KEY: VARIANT
286 <222> LOCATION: (10)
287 <223> OTHER INFORMATION: Wherein Xaa is any amino acid ✓
289 <220> FEATURE:
290 <221> NAME/KEY: VARIANT
291 <222> LOCATION: (14)
292 <223> OTHER INFORMATION: Wherein Xaa is any amino acid. ✓
294 <220> FEATURE:
295 <221> NAME/KEY: VARIANT ✓
296 <222> LOCATION: (17)..(18)
298 <220> FEATURE:
299 <221> NAME/KEY: VARIANT
300 <222> LOCATION: (25)..(26) ✓
301 <223> OTHER INFORMATION: Wherein Xaa is any amino acid. ✓
303 <220> FEATURE:
304 <221> NAME/KEY: VARIANT ✓
305 <222> LOCATION: (29)
306 <223> OTHER INFORMATION: Wherein Xaa is any amino acid.
308 <400> SEQUENCE: 4
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      310   1             5             10             15
W--> 312 Xaa Xaa Cys Asn Asn Ala Ala Cys Xaa Xaa Asp Gly Xaa Asp Cys
      313             20             25             30
316 <210> SEQ ID NO: 5
317 <211> LENGTH: 1242
318 <212> TYPE: PRT
319 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 5
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323   1             5             10             15
325 Gly Tyr Leu Arg Lys Pro Lys Ser Met His Lys Arg Phe Phe Val Leu
326             20             25             30
328 Arg Ala Ala Ser Glu Ala Gly Gly Pro Ala Arg Leu Glu Tyr Tyr Glu
329             35             40             45
331 Asn Glu Lys Lys Trp Arg His Lys Ser Ser Ala Pro Lys Arg Ser Ile
332   50             55             60

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VERIFICATION SUMMARY

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Input Set : A:\Rih32d31.app

Output Set: N:\CRF3\10302001\I903063.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:60 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:63 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4

L:312 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4